

Application No. : 09/872,761
 Docket No. : 340078.401

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Paragraph beginning at page 11, line 17, has been amended as follows:

A 205 base pair segment of the lacI gene with the sequence (SEQ ID NO:1):

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1      AATTCTATAAA GGAGATATCA TATGAAACCG GTAACGTAT ACGACGTCGC TGAATACGCC
61     GGC GTT CTT ACCAGACC GTT CTA GAG TG GTTA ACCAGG CTTCACATGT TAGCGCTAAA
121    ACC CGG GAAA AAG TTGAAGC TGCCATGGCT GAGCTCAACT ACATCCC GAA CCGT GTTGCG
181    CAGCAGCTGG CTGGTAAACA AAGCT
  
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is synthesized using a set of overlapping double-stranded oligonucleotides.

Paragraph beginning at page 14, line 12, has been amended as follows:

One common side reaction of oligonucleotide synthesis is the formation of diaminopurine from a dG residue in the DNA chain. Modified oligonucleotides containing 2,6-diaminopurine are obtained from Trilink Biotechnologies (San Diego, CA) and incorporated into the 205 bp lacI gene fragment. Four samples were prepared as described in Example 1, with one diaminopurine residue (labeled **D** below) substituted for a dG residue in each sample.

<u>Oligonucleotide</u>	<u>Fragment Name</u>	<u>Base Replaced</u>	<u>SEQ ID NO:</u>
5' ACCGTTCTADAGTGGTTAACCGG 3'	D-T86	86	<u>2</u>
5' ACCGTTCTAGADTGGTTAACCGG 3'	D-T88	88	<u>3</u>
5' GGAAAAADTTGAAGCTGCCATGGCT 3'	D-T133	133	<u>4</u>
5' TTDCGCAGCAGCTGGCTGGTAAACAA 3'	D-T178	178	<u>5</u>

Paragraph beginning at page 15, line 3, has been amended as follows:

A second common side reaction of oligonucleotide synthesis is deamination of the N4-amine of deoxycytidine to form a uracil (dU) in the DNA chain. Modified oligonucleotides containing uracil (dU) are obtained from Midland Certified Reagent Company (Midland, TX) and incorporated into the 205 bp lacI gene fragment. Two samples were prepared as described in Example 1, with one uracil residue (labeled dU below) substituted for a dC residue in each sample.

<u>Oligonucleotide</u>	<u>Fragment Name</u>	<u>Base Replaced</u>	<u>SEQ ID NO:</u>
5' TGAAGCCTGGTTAACCACT <u>dU</u> TAGAA 3'	U-B86	86	<u>6</u>
5' AGCTCAGCCATGGCAGCTTCAAdUTT 3'	U-B133	133	<u>7</u>

Paragraph beginning at page 15, line 13, has been amended as follows:

A third common side reaction of oligonucleotide synthesis is the formation of abasic sites by depurination of protected adenosine residues during chain elongation. Modified oligonucleotides containing uracil are obtained from Midland Certified Reagent Company (Midland, TX) and incorporated into the 205 bp lacI gene fragment. Two samples were prepared as described in Example 1, with one uracil residue (labeled dU below) substituted for a dA residue in each sample.

<u>Oligonucleotide</u>	<u>Fragment Name</u>	<u>Base Replaced</u>	<u>SEQ ID NO:</u>
5' AGCTCAGCCATGGCAGCTTCA <u>dU</u> CTT 3'	A-B134	134	<u>8</u>
5' TTGCGC <u>dU</u> GCAGCTGGCTGGTAAACAA 3'	A-T182	182	<u>9</u>

Paragraph beginning at page 16, line 7, has been amended as follows:

The thermal and gradient conditions for isolating chemically-pure enriched sequence are calculated using the DHPLC Melt Program (<http://insertion.stanford.edu/melt.html>) available from Stanford University (Palo Alto, CA) and available for license from the Stanford University Office of Technology Licensing referring to the docket number S95-024. The 4 base single-

stranded region on either end of the 205 base pair fragment is removed to give the following 197 base pair sequence (SEQ ID NO: 10).

lac I Region

CATAAAGGAGATATCATATGAAACCGGTAACGTTATACGACGTCGCTGAA
TACGCCGGCGTTCTTACCAGACCGTTCTAGAGTGGTTAACCAGGCTTC
ACATGTTAGCGCTAAAACCCGGGAAAAAGTTGAAGCTGCCATGGCTGAGC
TCAACTACATCCGAACCGTGTGCGCAGCAGCTGGCTGGTAAACAA

Paragraph beginning at page 20, line 14, has been amended as follows:

The control and the four sequences containing the synthesis byproducts are listed below:

5'- ATTGCCCTTGCCACTAACGCACCAGCGAAACGGTACTTACCGACACG-3' Control (SEQ ID NO:11)
5'-ATTGCCCTTGCCACTAACGCACCAGCGAAACGGTACT ACCGACACG-3' n-1 (SEQ ID NO:12)
5'-ATTGCCCTTGCCACTAACGCACCAGCGAAACGGTACTTTACCGACACG-3' n+ (SEQ ID NO:13)
5'-ATTGCCCTTGCCACTAACGCACCAGCGAAACGGTACTTGCCGACACG-3' T/G Mismatch
(SEQ ID NO:14)
5'-ATTGCCCTTGCCACTAACGCACCAGCGAAACGGTACTTGCGACACG-3' G/G Mismatch
(SEQ ID NO:15)